

Claims

1. DNA sequences which contain the coding region of an amino acid transporter, characterised in that the information contained in the nucleotide sequence allows, by integration in a plant genome, the formation of RNA, and with this RNA, a new amino acid transport activity can be introduced in the plant cells or an endogenous amino acid transporter activity can be expressed.
2. A DNA sequence according to claim 1, characterised in that, it contains the following nucleotide sequence (Seq-ID No 1):

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CTTAAACAT TTATTTTATC TTCTTCTTGT TCTCTCTTTC TCTTTCTCTC ATCACT   56

ATG AAG AGT TTC AAC ACA GAA GGA CAC AAC CAC TCC ACG GCG GAA   101
Met Lys Ser Phe Asn Thr Glu Gly His Asn His Ser Thr Ala Glu
1           5           10           15

TCC GGC GAT GCC TAC ACC GTG TCG GAC CCG ACA AAG AAC GTC GAT   146
Ser Gly Asp Ala Tyr Thr Val Ser Asp Pro Thr Lys Asn Val Asp
           20           25           30

GAA GAT GGT CGA GAG AAG CGT ACC GGG ACG TGG CTT ACG GCG AGT   191
Glu Asp Gly Arg Glu Lys Arg Thr Gly Thr Trp Leu Thr Ala Ser
           35           40           45

GCG CAT ATT ATC ACG GCG GTG ATA GGC TCC GGA GTG TTG TCT TTA   236
Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu
           50           55           60

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GCA TGG GCT ATA GCT CAG CTT GGT TGG ATC GCA GGG ACA TCG ATC	281
Ala Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Thr Ser Ile	
65 70 75	
TTA CTC ATT TTC TCG TTC ATT ACT TAC TTC ACC TCC ACC ATG CTT	326
Leu Leu Ile Phe Ser Phe Ile Thr Tyr Phe Thr Ser Thr Met Leu	
80 85 90	
GCC GAT TGC TAC CGT GCG CCG GAT CCC GTC ACC GGA AAA CGG AAT	371
Ala Asp Cys Tyr Arg Ala Pro Asp Pro Val Thr Gly Lys Arg Asn	
95 100 105	
TAC ACT TAC ATG GAC GTT GTT CGA TCT TAC CTC GGT GGT AGG AAA	416
Tyr Thr Tyr Met Asp Val Val Arg Ser Tyr Leu Gly Gly Arg Lys	
110 115 120	
GTG CAG CTC TGT GGA GTG GCA CAA TAT GGG AAT CTG ATT GGG GTC	461
Val Gln Leu Cys Gly Val Ala Gln Tyr Gly Asn Leu Ile Gly Val	
125 130 135	
ACT GTT GGT TAC ACC ATC ACT GCT TCT ATT AGT TTG GTA GCG GTA	506
Thr Val Gly Tyr Thr Ile Thr Ala Ser Ile Ser Leu Val Ala Val	
140 145 150	
GGG AAA TCG AAC TGC TTC CAC GAT AAA GGG CAC ACT GCG GAT TGT	551
Gly Lys Ser Asn Cys Phe His Asp Lys Gly His Thr Ala Asp Cys	
155 160 165	
ACT ATA TCG AAT TAT CCG TAT ATG GCG GTT TTT GGT ATC ATT CAA	596
Thr Ile Ser Asn Tyr Pro Tyr Met Ala Val Phe Gly Ile Ile Gln	
170 175 180	
GTT ATT CTT AGC CAG ATC CCA AAT TTC CAC AAG CTC TCT TTT CTT	641
Val Ile Leu Ser Gln Ile Pro Asn Phe His Lys Leu Ser Phe Leu	
185 190 195	

TCC	ATT	ATG	GCC	GCA	GTC	ATG	TCC	TTT	ACT	TAT	GCA	ACT	ATT	GGA	686
Ser	Ile	Met	Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ala	Thr	Ile	Gly	
			200						205					210	
ATC	GGT	CTA	GCC	ATC	GCA	ACC	GTC	GCA	GGT	GGG	AAA	GTG	GGT	AAG	731
Ile	Gly	Leu	Ala	Ile	Ala	Thr	Val	Ala	Gly	Gly	Lys	Val	Gly	Lys	
			215						220					225	
ACG	AGT	ATG	ACG	GGC	ACA	GCG	GTT	GGA	GTA	GAT	GTA	ACC	GCA	GCT	776
Thr	Ser	Met	Thr	Gly	Thr	Ala	Val	Gly	Val	Asp	Val	Thr	Ala	Ala	
				230					235					240	
CAA	AAG	ATA	TGG	AGA	TCG	TTT	CAA	GCG	GTT	GGG	GAC	ATA	GCG	TTC	821
Gln	Lys	Ile	Trp	Arg	Ser	Phe	Gln	Ala	Val	Gly	Asp	Ile	Ala	Phe	
				245					250					255	
GCC	TAT	GCT	TAT	GCC	ACG	GTT	CTC	ATC	GAG	ATT	CAG	GAT	ACA	CTA	866
Ala	Tyr	Ala	Tyr	Ala	Thr	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	
				260					265					270	
AGA	TCT	AGC	CCA	GCT	GAG	AAC	AAA	GCC	ATG	AAA	AGA	GCA	AGT	CTT	911
Arg	Ser	Ser	Pro	Ala	Glu	Asn	Lys	Ala	Met	Lys	Arg	Ala	Ser	Leu	
			-	275					280					285	
GTG	GGA	GTA	TCA	ACC	ACC	ACT	TTT	TTC	TAC	ATC	TTA	TGT	GGA	TGC	956
Val	Gly	Val	Ser	Thr	Thr	Thr	Phe	Phe	Tyr	Ile	Leu	Cys	Gly	Cys	
				290					295					300	
ATC	GGC	TAT	GCT	GCA	TTT	GGA	AAC	AAT	GCC	CCT	GGA	GAT	TTC	CTC	1001
Ile	Gly	Tyr	Ala	Ala	Phe	Gly	Asn	Asn	Ala	Pro	Gly	Asp	Phe	Leu	
				305					310					315	
ACA	GAT	TTC	GGG	TTT	TTC	GAG	CCC	TTT	TGG	CTC	ATT	GAC	TTT	GCA	1046
Thr	Asp	Phe	Gly	Phe	Phe	Glu	Pro	Phe	Trp	Leu	Ile	Asp	Phe	Ala	
				320					325					330	

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AAC GCT TGC ATC GCT GTC CAC CTT ATT GGT GCC TAT CAG GTG TTC 1091
 Asn Ala Cys Ile Ala Val His Leu Ile Gly Ala Tyr Gln Val Phe
 335 340 345

GCG CAG CCG ATA TTC CAG TTT GTT GAG AAA AAA TGC AAC AGA AAC 1136
 Ala Gln Pro Ile Phe Gln Phe Val Glu Lys Lys Cys Asn Arg Asn
 350 355 360

TAT CCA GAC AAC AAG TTC ATC ACT TCT GAA TAT TCA GTA AAC GTA 1181
 Tyr Pro Asp Asn Lys Phe Ile Thr Ser Glu Tyr Ser Val Asn Val
 365 370 375

CCT TTC CTT GGA AAA TTC AAC ATT AGC CTC TTC AGA TTG GTG TGG 1226
 Pro Phe Leu Gly Lys Phe Asn Ile Ser Leu Phe Arg Leu Val Trp
 380 385 390

AGG ACA GCT TAT GTG GTT ATA ACC ACT GTT GTA GCT ATG ATA TTC 1271
 Arg Thr Ala Tyr Val Val Ile Thr Thr Val Val Ala Met Ile Phe
 395 400 405

CCT TTC TTC AAC GCG ATC TTA GGT CTT ATC GGA GCA GCT TCC TTC 1316
 Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly Ala Ala Ser Phe
 410 415 420

TGG CCT TTA ACG GTT TAT TTC CCT GTG GAG ATG CAC ATT GCA CAA 1361
 Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met His Ile Ala Gln
 425 430 435

ACC AAG ATT AAG AAG TAC TCT GCT AGA TGG ATT GCG CTG AAA ACG 1406
 Thr Lys Ile Lys Lys Tyr Ser Ala Arg Trp Ile Ala Leu Lys Thr
 440 445 450

ATG TGC TAT GTT TGC TTG ATC GTC TCG CTC TTA GCT GCA GCC GGA 1451
 Met Cys Tyr Val Cys Leu Ile Val Ser Leu Leu Ala Ala Ala Gly
 455 460 465

0985474-051401

TCC ATC GCA GGA CTT ATA AGT AGT GTC AAA ACC TAC AAG CCC TTC 1496
 Ser Ile Ala Gly Leu Ile Ser Ser Val Lys Thr Tyr Lys Pro Phe
 470 475 480

CGG ACT ATG CAT GAG TGAGTTTGAG ATCCTCAAGA GAGTCAAAAA 1541
 Arg Thr Met His Glu
 485

TATATGTAGT AGTTTGGTCT TTCTGTTAAA CTATCTGGTG TCTAAATCCA 1591

ATGAGAATGC TTTATTGCTA AAACCTCATG AATCTCTCTG TATCTACATC 1641

TTTCAATCTA ATACATATGA GCTCTTCCAA AAAAAAAAAA AAAA 1685

3. A DNA sequence according to claim 1, characterised in that it contains the following nucleotide sequence (Seq-ID No 2):

CTATTTTAT AATTCCTCTT CTTTTTGTTT 29

ATAGCTTTGT AATTATAGTC TTATTTCTCT TTAAGGCTCA ATAAGAGGAG 79

ATG GGT GAA ACC GCT GCC GCC AAT AAC CAC CGT CAC CAC CAC CAT 124
 Met Gly Glu Thr Ala Ala Ala Asn Asn His Arg His His His His
 1 5 10 15

CAC GGC CAC CAG GTC TTT GAC GTG GCC AGC CAC GAT TTC GTC CCT 169
 His Gly His Gln Val Phe Asp Val Ala Ser His Asp Phe Val Pro
 20 25 30

CCA CAA CCG GCT TTT AAA TGC TTC GAT GAT GAT GGC CGC CTC AAA 214
 Pro Gln Pro Ala Phe Lys Cys Phe Asp Asp Asp Gly Arg Leu Lys
 35 40 45

AGA ACT GGG ACT GTT TGG ACC GCG AGC GCT CAT ATA ATA ACT GCG 259
 Arg Thr Gly Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala
 50 55 60

GTT ATC GGA TCC GGC GTT TTG TCA TTG GCG TGG GCG ATT GCA CAG 304
 Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln
 65 70 75

CTC GGA TGG ATC GCT GGC CCT GCT GTG ATG CTA TTG TTC TCT CTT 349
 Leu Gly Trp Ile Ala Gly Pro Ala Val Met Leu Leu Phe Ser Leu
 80 85 90

GTT ACT CTT TAC TCC TCC ACA CTT CTT AGC GAC TGC TAC AGA ACC 394
 Val Thr Leu Tyr Ser Ser Thr Leu Leu Ser Asp Cys Tyr Arg Thr
 95 100 105

GGC GAT GCA GTG TCT GGC AAG AGA AAC TAC ACT TAC ATG GAT GCC 439
 Gly Asp Ala Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala
 110 115 120

GTT CGA TCA ATT CTC GGT GGG TTC AAG TTC AAG ATT TGT GGG TTG 484
 Val Arg Ser Ile Leu Gly Gly Phe Lys Phe Lys Ile Cys Gly Leu
 125 130 135

ATT CAA TAC TTG AAT CTC TTT GGT ATC GCA ATT GGA TAC ACG ATA 529
 Ile Gln Tyr Leu Asn Leu Phe Gly Ile Ala Ile Gly Tyr Thr Ile
 140 145 150

GCA GCT TCC ATA AGC ATG ATG GCG ATC AAG AGA TCC AAC TGC TTC 574
 Ala Ala Ser Ile Ser Met Met Ala Ile Lys Arg Ser Asn Cys Phe
 155 160 165

CAC AAG AGT GGA GGA AAA GAC CCA TGT CAC ATG TCC AGT AAT CCT 619
 His Lys Ser Gly Gly Lys Asp Pro Cys His Met Ser Ser Asn Pro
 170 175 180

TAC ATG ATC GTA TTT GGT GTG GCA GAG ATC TTG CTC TCT CAG GTT	664
Tyr Met Ile Val Phe Gly Val Ala Glu Ile Leu Leu Ser Gln Val	
185 190 200	
CCT GAT TTC GAT CAG ATT TGG TGG ATC TCC ATT GTT GCA GCT GTT	709
Pro Asp Phe Asp Gln Ile Trp Trp Ile Ser Ile Val Ala Ala Val	
205 210 220	
ATG TCC TTC ACT TAC TCT GCC ATT GGT CTA GCT CTT GGA ATC GTT	754
Met Ser Phe Thr Tyr Ser Ala Ile Gly Leu Ala Leu Gly Ile Val	
225 230 235	
CAA GTT GCA GCG AAT GGA GTT TTC AAA GGA AGT CTC ACT GGA ATA	799
Gln Val Ala Ala Asn Gly Val Phe Lys Gly Ser Leu Thr Gly Ile	
240 245 250	
AGC ATC GGA ACA GTG ACT CAA ACA CAG AAG ATA TGG AGA ACC TTC	844
Ser Ile Gly Thr Val Thr Gln Thr Gln Lys Ile Trp Arg Thr Phe	
255 260 265	
CAA GCA CTT GGA GAC ATT GCC TTT GCG TAC TCA TAC TCT GTT GTC	889
Gln Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Val Val	
270 275 280	
CTA ATC GAG ATT CAG GAT ACT GTA AGA TCC CCA CCG GCG GAA TCG	934
Leu Ile Glu Ile Gln Asp Thr Val Arg Ser Pro Pro Ala Glu Ser	
285 290 295	
AAA ACG ATG AAG AAA GCA ACA AAA ATC AGT ATT GCC GTC ACA ACT	979
Lys Thr Met Lys Lys Ala Thr Lys Ile Ser Ile Ala Val Thr Thr	
300 305 310	
ATC TTC TAC ATG CTA TGT GGC TCA ATG GGT TAT GCC GCT TTT GGA	1024
Ile Phe Tyr Met Leu Cys Gly Ser Met Gly Tyr Ala Ala Phe Gly	
315 320 325	

TTT CCG GTG GAG ATG TAT ATT AAG CAG AGG AAG GTT GAG AAA TGG 1429
Phe Pro Val Glu Met Tyr Ile Lys Gln Arg Lys Val Glu Lys Trp
450 455 460

AGC ACG AGA TGG GTG TGT TTA CAG ATG CTT AGT GTT GCT TGT CTT 1474
 Ser Thr Arg Trp Val Cys Leu Gln Met Leu Ser Val Ala Cys Leu
 465 470 475

GTG ATC TCG GTG GTC GCC GGG GTT GGA TCA ATC GCC GGA GTG ATG 1519
 Val Ile Ser Val Val Ala Gly Val Gly Ser Ile Ala Gly Val Met
 480 485 490

CTT GAT CTT AAG GTC TAT AAG CCA TTC AAG TCT ACA TAT 1558
 Leu Asp Leu Lys Val Tyr Lys Pro Phe Lys Ser Thr Tyr
 495 500

TGATGATTAT GGACCATGAA CAACAGAGAG AGTTGGTGTG TAAAGTTTAC 1608

CATTTCAAAG AAAACTCCAA AAATGTGTAT ATTGTATGTT GTTCTCATT 1658

CGTATGGTCT CATCTTTGTA ATAAATTTA AACTTATGT TATAAATTAT 1708

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 1740

4. A plasmid, characterised in that it contains a DNA sequence according to any one of claims 1 to 3.
5. Plasmid pPPP1-20 (DSM 7129).
6. Plasmid pAAP2, prepared according to Example 2.
7. Plasmid pBin PPP1-20 (DSM 7130).
- 10 8. Use of the plasmid according to any one of claims 4 to 7 or derivatives or parts thereof, for the transformation of prokaryotic and eukaryotic cells.
9. Plants containing a DNA sequence according to any one of claims 1 to 3.

10. Bacteria containing a DNA sequence according to any one of claims 1 to 3.
- 5 11. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the preparation of plasmids with changed specificity of the transporter.
- 10 12. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for isolation of similar sequences from the genome of the plant.
- 15 13. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the expression of translatable mRNA, that makes possible the synthesis of an amino acid transporter in prokaryotic and eukaryotic cells.
- 20 14. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the expression of a non-translatable mRNA, that hinders the synthesis of an amino acid transporter in prokaryotic and eukaryotic cells.
- 25 15. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 in combination with steering elements for an expression in prokaryotic and eukaryotic cells.
- 30 16. Yeast strains containing DNA sequences according to any one of claims 1 to 3.
- 35 17. Use of yeast strains containing DNA sequences according to claim 16 for identification of a plant amino acid transporter.

18. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for preparation of plants with changed amino acid and nitrogen metabolism.

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19. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for preparation of crop plants with increased yield.

10 20. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the transport of compounds in prokaryotic and eukaryotic cells.

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